

SEQUENZPROTOKOLL

<110> Henkel Kommanditgesellschaft auf Aktien

<120> Wasch- und Reinigungsmittel mit Hybrid-Alpha-Amylasen

<130> H 4714 PCT

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<150> DE 10138753.9-41

<151> 2001-08-07

<160> 18

<170> PatentIn Ver. 2.1

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<211> 1452

<212> DNA

<213> Bacillus licheniformis

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gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga	144
Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly	
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Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu	
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Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn	
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gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc	336
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Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val	
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Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val 115 120 125
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 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
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 Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
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 His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
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Val Gln Lys

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<210> 5
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 <213> Künstliche Sequenz

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amyloliquefaciens (AL34).

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 Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
 180 185 190
 Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
 195 200 205
 Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
 210 215 220
 Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
 225 230 235 240
 Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
 245 250 255
 Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
 260 265 270
 Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
 275 280 285
 Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
 290 295 300
 Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
 305 310 315 320
 Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
 325 330 335
 Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
 340 345 350
 Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
 355 360 365
 Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
 370 375 380
 Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
 385 390 395 400
 Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
 405 410 415
 Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
 420 425 430
 Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
 435 440 445
 Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
 450 455 460
 Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
 465 470 475 480
 Arg

<210> 7

<211> 1446

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylas -Gene von B. licheniformis und B.
 amyloliquefaciens (AL76).

<220>

<221> CDS

<222> (1)..(1446)

<400> 7

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gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac   48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
  1             5             10             15

ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat   96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
             20             25             30

atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc   144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
             35             40             45

caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa   192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
             50             55             60

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa gga gag   240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
             65             70             75             80

ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac gtt tac   288
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
             85             90             95

ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc gaa gat   336
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
             100            105            110

gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca   384
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
             115            120            125

gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc   432
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
             130            135            140

ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt gac gga   480
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
             145            150            155            160

acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag ttt caa   528
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
             165            170            175

gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac tat gat   576
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
             180            185            190

tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc gca gca   624
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
             195            200            205

gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa ttg gac   672
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
             210            215            220

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ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt ttg cgg	720
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg	
225 230 235 240	
gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg ttt acg	768
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr	
245 250 255	
gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac tat ttg	816
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu	
260 265 270	
aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt cat tat	864
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr	
275 280 285	
cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg agg aaa	912
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys	
290 295 300	
ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg gtt aca	960
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr	
305 310 315 320	
ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act	1008
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr	
325 330 335	
gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg	1056
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg	
340 345 350	
gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa	1104
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys	
355 360 365	
gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg	1152
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro	
370 375 380	
atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat	1200
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr	
385 390 395 400	
ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg	1248
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser	
405 410 415	
gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg	1296
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly	
420 425 430	
gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat	1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His	
435 440 445	
gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc	1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly	

450	455	460	
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa			1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln			
465	470	475	480

aga tag			1446
Arg			

<210> 8

<211> 481

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL76).

<400> 8

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
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Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr	
85 90 95	
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser	
115 120 125	
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg	
130 135 140	
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln	
165 170 175	
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp	
180 185 190	
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala	
195 200 205	
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp	
210 215 220	
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg	
225 230 235 240	
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr	
245 250 255	
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu	
260 265 270	
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr	
275 280 285	
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys	
290 295 300	
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr	
305 310 315 320	

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Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
              325              330              335
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
              340              345              350
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
              355              360              365
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
              370              375              380
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
385              390              395              400
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
              405              410              415
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
              420              425              430
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
              435              440              445
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
              450              455              460
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465              470              475              480
Arg

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<210> 9

<211> 1446

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL112).

<220>

<221> CDS

<222> (1) .. (1446)

<400> 9

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gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac      48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
   1              5              10              15

ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat      96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
              20              25              30

atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc      144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
              35              40              45

caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa      192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
              50              55              60

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag      240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
   65              70              75              80

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ctt	caa	gat	gcg	atc	ggc	tca	ctg	cat	tcc	cgg	aac	gtc	caa	gta	tac	288
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				85					90					95		
gga	gat	gtg	gtt	ttg	aat	cat	aag	gct	ggg	gct	gat	gca	aca	gaa	gat	336
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
			100					105					110			
gta	acc	gcg	gtt	gaa	gtc	gat	ccc	gct	gac	cgc	aac	cgc	gta	att	tca	384
Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser	
			115				120					125				
gga	gaa	cac	cga	att	aaa	gcc	tgg	aca	cat	ttt	cat	ttt	ccg	ggg	cgc	432
Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg	
	130					135					140					
ggc	agc	aca	tac	agc	gat	ttt	aaa	tgg	cat	tgg	tac	cat	ttt	gac	gga	480
Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	
145					150					155					160	
acc	gat	tgg	gac	gag	tcc	cga	aag	ctg	aac	cgc	atc	tat	aag	ttt	caa	528
Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln	
				165					170					175		
gga	aag	gct	tgg	gat	tgg	gaa	gtt	tcc	aat	gaa	aac	ggc	aac	tat	gat	576
Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	
			180					185					190			
tat	ttg	atg	tat	gcc	gac	atc	gat	tat	gac	cat	cct	gat	gtc	gca	gca	624
Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	
		195					200					205				
gaa	att	aag	aga	tgg	ggc	act	tgg	tat	gcc	aat	gaa	ctg	caa	ttg	gac	672
Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	
	210					215					220					
ggg	ttc	cgt	ctt	gat	gct	gtc	aaa	cac	att	aaa	ttt	tct	ttt	ttg	cgg	720
Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	
225					230					235					240	
gat	tgg	gtt	aat	cat	gtc	agg	gaa	aaa	acg	ggg	aag	gaa	atg	ttt	acg	768
Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr	
				245					250					255		
gta	gct	gaa	tat	tgg	cag	aat	gac	ttg	ggc	gcg	ctg	gaa	aac	tat	ttg	816
Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu	
			260					265					270			
aac	aaa	aca	aat	ttt	aat	cat	tca	gtg	ttt	gac	gtg	ccg	ctt	cat	tat	864
Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	
		275					280					285				
cag	ttc	cat	gct	gca	tcg	aca	cag	gga	ggc	ggc	tat	gat	atg	agg	aaa	912
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys	
	290					295					300					
ttg	ctg	aac	agt	acg	gtc	gtt	tcc	aag	cat	ccg	ttg	aaa	gcg	gtt	aca	960
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr	
305					310					315					320	


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ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act 1008
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
          325                      330                      335

gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg 1056
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
          340                      345                      350

gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa 1104
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
          355                      360                      365

gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg 1152
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
          370                      375                      380

atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat 1200
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
          385                      390                      395                      400

ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg 1248
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
          405                      410                      415

gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg 1296
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
          420                      425                      430

gca aag cga atg tat gtc ggc ccg caa aac gcc ggt gag aca tgg cat 1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
          435                      440                      445

gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc 1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
          450                      455                      460

tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa 1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
          465                      470                      475                      480

aga tag 1446
Arg

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<210> 10

<211> 481

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL112).

<400> 10

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Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1              5              10              15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
          20              25              30
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser

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35						40						45					
Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu		
Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ser	Glu		
Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr		
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp		
Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser		
Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg		
Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly		
Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln		
Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp		
Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala		
Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp		
Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg		
Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr		
Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu		
Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr		
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys		
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr		
Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr		
Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg		
Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys		
Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro		
Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr		
Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser		
Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly		
Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His		
Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly		
Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln		
Arg																	

<210> 11
 <211> 1452
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von *B. licheniformis* und *B.*
amyloliquefaciens (AL256).

<220>
 <221> CDS
 <222> (1)..(1452)

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 ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat 96
 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20 25 30
 atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45
 caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa 192
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag 240
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65 70 75 80
 ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac 288
 Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
 85 90 95
 gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat 336
 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
 100 105 110
 gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg 384
 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
 115 120 125
 gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt 432
 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
 130 135 140
 gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga 480
 Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
 145 150 155 160
 gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt 528
 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
 165 170 175

ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac	576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn	
180 185 190	
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc	624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val	
195 200 205	
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca	672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser	
210 215 220	
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt	720
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe	
225 230 235 240	
ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg	768
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met	
245 250 255	
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac	816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn	
260 265 270	
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt	864
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu	
275 280 285	
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg	912
His Tyr Gln Phe His Ala Ser Thr Gln Gly Gly Tyr Asp Met	
290 295 300	
agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg	960
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala	
305 310 315 320	
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag	1008
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu	
325 330 335	
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc	1056
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu	
340 345 350	
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg	1104
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly	
355 360 365	
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att	1152
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile	
370 375 380	
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat	1200
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His	
385 390 395 400	
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac	1248
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp	
405 410 415	

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agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc 1296
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
      420                      425                      430

ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca 1344
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
      435                      440                      445

tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg 1392
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
      450                      455                      460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1440
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465                      470                      475                      480

ggt caa aga tag 1452
Val Gln Arg

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<210> 12

<211> 483

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz:Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL256).

<400> 12

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Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1      5      10      15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
      20      25      30
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
      35      40      45
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
      50      55      60
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
      65      70      75      80
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
      85      90      95
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
      100      105      110
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
      115      120      125
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
      130      135      140
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145      150      155      160
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
      165      170      175
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
      180      185      190
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
      195      200      205
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210      215      220
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe

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225		230		235		240									
Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met
				245					250					255	
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn
			260					265					270		
Tyr	Leu	Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu
		275					280					285			
His	Tyr	Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met
	290					295				300					
Arg	Lys	Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala
305				310						315					320
Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu
			325						330					335	
Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
			340					345					350		
Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly
		355					360					365			
Thr	Lys	Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile
	370					375					380				
Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His
385				390						395					400
Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp
			405						410					415	
Ser	Ser	Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
			420					425					430		
Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr
		435					440					445			
Trp	His	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser
	450					455				460					
Glu	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr
465				470						475					480
Val	Gln	Arg													

<210> 13

<211> 1452

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (ALA34-84).

<220>

<221> CDS

<222> (1)..(1452)

<400> 13

gta	aat	ggc	acg	ctg	atg	cag	tat	ttt	gaa	tgg	tat	acg	ccg	aac	gac	48
Val	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Thr	Pro	Asn	Asp	
1				5					10					15		

ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	tcg	gat	96
Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
		20					25						30			

atc	ggt	att	act	gcc	gtc	tgg	att	ccc	ccg	gca	tat	aag	gga	acg	agc	144
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Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser	
35 40 45	
caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta ggg gag	192
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa gga gag	240
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
ctg caa tct gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac	288
Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat	336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg	384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	
115 120 125	
gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt	432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	
130 135 140	
gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga	480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt	528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg	
165 170 175	
ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac	576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn	
180 185 190	
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc	624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val	
195 200 205	
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca	672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser	
210 215 220	
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt	720
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe	
225 230 235 240	
ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg	768
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met	
245 250 255	
ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac	816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn	
260 265 270	

tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt	864
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu	
275 280 285	
cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat atg	912
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met	
290 295 300	
agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg	960
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala	
305 310 315 320	
gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg gaa	1008
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu	
325 330 335	
tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg	1056
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu	
340 345 350	
aca aga gaa tcc ggt tat cct cag gtg ttc tat ggg gat atg tac ggg	1104
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly	
355 360 365	
aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat aat ata	1152
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile	
370 375 380	
gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc cag cac	1200
Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His	
385 390 395 400	
gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa ggt gac	1248
Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp	
405 410 415	
agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac gga ccc	1296
Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	
420 425 430	
ggc gga tca aag cgg atg tat gcc ggc ctg aaa aat gcc ggc gag aca	1344
Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr	
435 440 445	
tgg tat gac ata acg ggc aac cgt tca gat act gta aaa atc gga tct	1392
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser	
450 455 460	
gac ggc tgg gga gag ttt cat gta aac gat ggg tcc gtc tcc att tat	1440
Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr	
465 470 475 480	
gtt cag aaa taa	1452
Val Gln Lys	

<210> 14

<211> 483

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (ALA34-84).

<400> 14

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Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1           5           10           15
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          20           25           30
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
      35           40           45
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
      50           55           60
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
      65           70           75           80
Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
          85           90           95
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
      100           105           110
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
      115           120           125
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
      130           135           140
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
      145           150           155           160
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
          165           170           175
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
      180           185           190
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
      195           200           205
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
      210           215           220
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
      225           230           235           240
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
          245           250           255
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
      260           265           270
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
      275           280           285
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Tyr Asp Met
      290           295           300
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
      305           310           315           320
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
          325           330           335
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
      340           345           350
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
      355           360           365
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
      370           375           380
Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
      385           390           395           400
Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
          405           410           415
Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro

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      420      425      430
Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
      435      440      445
Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
      450      455      460
Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465      470      475      480
Val Gln Lys

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<210> 15
 <211> 1458
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-433).

<220>
 <221> CDS
 <222> (1)..(1458)

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 1 5 10 15
 aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta 96
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
 20 25 30
 tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga 144
 Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta 192
 Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
 50 55 60
 gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa 240
 Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa 288
 Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
 85 90 95
 gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca 336
 Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
 100 105 110
 gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa 384
 Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
 115 120 125
 act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg 432

Thr	Ser	Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	
130						135					140					
ggc	cgt	gga	aac	acg	tac	agt	gat	ttt	aaa	tgg	cat	tgg	tat	cat	ttc	480
Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	
145					150					155					160	
gac	gga	gcg	gac	tgg	gat	gaa	tcc	cgg	aag	atc	agc	cgc	atc	ttt	aag	528
Asp	Gly	Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	
				165					170					175		
ttt	cgt	ggg	gaa	gga	aaa	gcg	tgg	gat	tgg	gaa	gta	tca	agt	gaa	aac	576
Phe	Arg	Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	
			180					185					190			
ggc	aac	tat	gac	tat	tta	atg	tat	gct	gat	gtt	gac	tac	gac	cac	cct	624
Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	
		195					200					205				
gat	gtc	gtg	gca	gag	aca	aaa	aaa	tgg	ggt	atc	tgg	tat	gcg	aat	gaa	672
Asp	Val	Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	
	210					215					220					
ctg	tca	tta	gac	ggc	ttc	cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	720
Leu	Ser	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	
225					230					235					240	
tca	ttt	ctg	cgt	gat	tgg	gtt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	768
Ser	Phe	Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	
				245					250					255		
gaa	atg	ttt	acg	gtt	gcg	gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	816
Glu	Met	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	
			260					265					270			
gaa	aac	tac	ttg	aat	aaa	aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	864
Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	
		275					280					285				
ccg	ctt	cat	ttc	aat	tta	cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	912
Pro	Leu	His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	
	290					295					300					
gat	atg	agg	cgt	ttg	ctg	gac	ggt	acc	gtt	gtg	tcc	agg	cat	ccg	gaa	960
Asp	Met	Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	
305					310					315					320	
aag	gcg	gtt	aca	ttt	gtt	gaa	aat	cat	gac	aca	cag	ccg	gga	cag	tca	1008
Lys	Ala	Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	
				325					330					335		
ttg	gaa	tcg	aca	gtc	caa	act	tgg	ttt	aaa	ccg	ctt	gca	tac	gcc	ttt	1056
Leu	Glu	Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	
			340					345					350			
att	ttg	aca	aga	gaa	tcc	ggt	tat	cct	cag	gtg	ttc	tat	ggg	gat	atg	1104
Ile	Leu	Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	
		355					360					365				

tac ggg aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat 1152
 Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp
 370 375 380

aat ata gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc 1200
 Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro
 385 390 395 400

cag cac gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa 1248
 Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu
 405 410 415

ggt gac agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac 1296
 Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp
 420 425 430

gga ccc ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt 1344
 Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly
 435 440 445

gag aca tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc 1392
 Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile
 450 455 460

aat tcg gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca 1440
 Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser
 465 470 475 480

att tat gtt caa aga tag 1458
 Ile Tyr Val Gln Arg
 485

<210> 16

<211> 485

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-433).

<400> 16

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
 20 25 30
 Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
 50 55 60
 Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
 85 90 95
 Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
 100 105 110
 Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
 115 120 125
 Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro

130		135		140
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe				
145		150		155
Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys				160
		165		170
Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn				175
		180		185
Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro				190
		195		200
Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu				205
		210		215
Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe				220
		225		230
Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys				235
		245		250
Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu				255
		260		265
Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val				270
		275		280
Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr				285
		290		295
Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu				300
		305		310
Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser				315
		325		330
Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe				335
		340		345
Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met				350
		355		360
Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp				365
		370		375
Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro				380
		385		390
Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu				395
		405		410
Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp				415
		420		425
Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly				430
		435		440
Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile				445
		450		455
Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser				460
		465		470
Ile Tyr Val Gln Arg				475
		485		480

<210> 17

<211> 1452

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylas -Gene von B. licheniformis und B.
amyloliquefaciens (LAL19-153).

<220>

<221> CDS

<222> (1)..(1452)

<400> 17

gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc	48
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro	
1 5 10 15	
aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta	96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu	
20 25 30	
tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga	144
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly	
35 40 45	
ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta	192
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu	
50 55 60	
gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa	240
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys	
65 70 75 80	
tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa	288
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln	
85 90 95	
gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca	336
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr	
100 105 110	
gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa	384
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu	
115 120 125	
act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg	432
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro	
130 135 140	
ggc cgt gga aac acg tac agt gat ttt aaa tgg cat tgg tac cat ttt	480
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe	
145 150 155 160	
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag	528
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys	
165 170 175	
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac	576
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn	
180 185 190	
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc	624
Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val	
195 200 205	
gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa	672
Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln	
210 215 220	

ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt	720
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe	
225 230 235 240	
ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg	768
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met	
245 250 255	
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac	816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn	
260 265 270	
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt	864
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu	
275 280 285	
cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg	912
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met	
290 295 300	
agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg	960
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala	
305 310 315 320	
ggt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag	1008
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu	
325 330 335	
tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc	1056
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu	
340 345 350	
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg	1104
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly	
355 360 365	
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att	1152
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile	
370 375 380	
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat	1200
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His	
385 390 395 400	
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac	1248
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp	
405 410 415	
agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc	1296
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	
420 425 430	
ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca	1344
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr	
435 440 445	
tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg	1392
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser	

450	455	460	
gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1440			
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr			
465	470	475	480

ggt caa aga tag	1452
Val Gln Arg	

<210> 18

<211> 483

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (LAL19-153).

<400> 18

Ala	Asn	Leu	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Met	Pro
1				5					10					15	
Asn	Asp	Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu
		20						25					30		
Ser	Asp	Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly
		35					40					45			
Leu	Ser	Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu
	50					55					60				
Gly	Glu	Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys
65				70					75						80
Ser	Glu	Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln
			85					90					95		
Val	Tyr	Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr
		100						105					110		
Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu
	115					120						125			
Thr	Ser	Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro
	130				135						140				
Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe
145				150					155						160
Asp	Gly	Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys
			165						170				175		
Phe	Gln	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn
		180						185				190			
Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val
	195					200						205			
Ala	Ala	Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln
	210					215					220				
Leu	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe
225				230					235						240
Leu	Arg	Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met
			245						250				255		
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn
		260					265						270		
Tyr	Leu	Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu
	275					280						285			
His	Tyr	Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met
	290				295						300				
Arg	Lys	Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala
305				310						315					320

[illegible]